

# SEQUENCE LISTING

<110> Olsen et al.

<120> Stanniocalcin Polynucleotides, Polypeptides, and Methods Based Thereon

<130> PF108P2

<140> US 09/840,989

<141> 2001-04-25

<150> PCT/US00/29432

<151> 2000-10-26

<150> US 60/161,740

<151> 1999-10-27

<160> 12

<170> PatentIn version 3.1

<210> 1

<211> 1283

<212> DNA

<213> Homo sapiens.

<220>

<221> CDS

<222> (45)..(788)

<223>

<220>

<221> misc\_feature

<222> (857)..(857)

<223> n is equal to a, t, c, or g.

<220>

<221> misc\_feature

<222> (1254)..(1254)

<223> n is equal to a, t, c, or g.

<220>

<221> misc\_feature

<222> (1279)..(1279)

<223> n is equal to a, t, c, or g.

<400> . 1

aaaaaaaaaa aaaacccaac aacttagcgg aaactttctca gaga atg ctc caa aac 56

Met Leu Gln Asn

1

tca gca gtg ctt ctg gtg ctg gtg atc agt gct tct gca acc cat gag 104

Ser Ala Val Leu Leu Val Leu Val Ile Ser Ala Ser Ala Thr His Glu

5 10 15 20

gcg gag cag aat gac tct gtg agc ccc agg aaa tcc cga gtg gcg gcc Ala Glu Gln Asn Asp Ser Val Ser Pro Arg Lys Ser Arg Val Ala Ala 25 30 35	152
caa aac tca gct gaa gtg gtt cgt tgc ctc aac agt gct cta cag gtc Gln Asn Ser Ala Glu Val Val Arg Cys Leu Asn Ser Ala Leu Gln Val 40 45 50	200
ggc tgc ggg gct ttt gca tgc ctg gaa aac tcc acc tgt gac aca gat Gly Cys Gly Ala Phe Ala Cys Leu Glu Asn Ser Thr Cys Asp Thr Asp 55 60 65	248
ggg atg tat gac atc tgt aaa tcc ttc ttg tac agc gct gct aaa ttt Gly Met Tyr Asp Ile Cys Lys Ser Phe Leu Tyr Ser Ala Ala Lys Phe 70 75 80	296
gac act cag gga aaa gca ttc gtc aaa gag agc tta aaa tgc atc gcc Asp Thr Gln Gly Lys Ala Phe Val Lys Glu Ser Leu Lys Cys Ile Ala 85 90 95 100	344
aac ggg gtc acc tcc aag gtc ttc ctc gcc att cgg agg tgc tcc act Asn Gly Val Thr Ser Lys Val Phe Leu Ala Ile Arg Arg Cys Ser Thr 105 110 115	392
ttc caa agg atg att gct gag gtg cag gaa gag tgc tac agc aag ctg Phe Gln Arg Met Ile Ala Glu Val Gln Glu Glu Cys Tyr Ser Lys Leu 120 125 130	440
aat gtg tgc agc atc gcc aag cgg aac cct gaa gcc atc act gag gtc Asn Val Cys Ser Ile Ala Lys Arg Asn Pro Glu Ala Ile Thr Glu Val 135 140 145	488
gtc cag ctg ccc aat cac ttc tcc aac aga tac tat aac aga ctt gtc Val Gln Leu Pro Asn His Phe Ser Asn Arg Tyr Tyr Asn Arg Leu Val 150 155 160	536
cga agc ctg ctg gaa tgt gat gaa gac aca gtc agc aca atc aga gac Arg Ser Leu Leu Glu Cys Asp Glu Asp Thr Val Ser Thr Ile Arg Asp 165 170 175 180	584
agc ctg atg gag aaa att ggg cct aac atg gcc agc ctc ttc cac atc Ser Leu Met Glu Lys Ile Gly Pro Asn Met Ala Ser Leu Phe His Ile 185 190 195	632
ctg cag aca gac cac tgt gcc caa aca cac cca cga gct gac ttc aac Leu Gln Thr Asp His Cys Ala Gln Thr His Pro Arg Ala Asp Phe Asn 200 205 210	680
agg aga cgc acc aat gag ccg cag aag ctg aaa gtc ctc ctc agg aac Arg Arg Arg Thr Asn Glu Pro Gln Lys Leu Lys Val Leu Leu Arg Asn 215 220 225	728
ctc cga ggt gag gag gac tct ccc tcc cac atc aaa cgc aca tcc cat Leu Arg Gly Glu Glu Asp Ser Pro Ser His Ile Lys Arg Thr Ser His 230 235 240	776
gag agt gca taa ccagggagag gttattcaca acctcaccaa actagtatca Glu Ser Ala 245	828

ttttaggggt gttgacacac cagttttgng tgtactgtgc ctggtttggt ttttttaaag	838
tagttcctat tttctatccc ccttaaagaa aattgcatga aactaggctt ctgtaatcaa	948
tatcccaaca ttctgcaatg ggaggattcc caccaacaaa atccatgtga acattcttgc	1008
tctcctcagg agaaagtacc ctctttttac caacttcctc tgccatgttt ttcccctgct	1068
cccctgagac ccccccaaa cacaaaaacat tcatgtaact ctccagccat tgtaatttga	1128
agatgtggat cccttttagaa acggttgccc cagtagagtt agctgataag gaaactttat	1188
ttaaatgcat gtcttaaagt ctcataaaga tgttaaattgg aattcgtgtt atgaatctgt	1248
gctggncatg gacgaaaaaa aaaaaaaaaa naaaa	1283

<210> 2  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Met	Leu	Gln	Asn	Ser	Ala	Val	Leu	Leu	Val	Leu	Val	Ile	Ser	Ala	Ser
1				5					10					15	

Ala	Thr	His	Glu	Ala	Glu	Gln	Asn	Asp	Ser	Val	Ser	Pro	Arg	Lys	Ser
			20					25					30		

Arg	Val	Ala	Ala	Gln	Asn	Ser	Ala	Glu	Val	Val	Arg	Cys	Leu	Asn	Ser
	35						40					45			

Ala	Leu	Gln	Val	Gly	Cys	Gly	Ala	Phe	Ala	Cys	Leu	Glu	Asn	Ser	Thr
	50					55					60				

Cys	Asp	Thr	Asp	Gly	Met	Tyr	Asp	Ile	Cys	Lys	Ser	Phe	Leu	Tyr	Ser
65					70					75				80	

Ala	Ala	Lys	Phe	Asp	Thr	Gln	Gly	Lys	Ala	Phe	Val	Lys	Glu	Ser	Leu
				85					90					95	

Lys	Cys	Ile	Ala	Asn	Gly	Val	Thr	Ser	Lys	Val	Phe	Leu	Ala	Ile	Arg
			100						105				110		

Arg	Cys	Ser	Thr	Phe	Gln	Arg	Met	Ile	Ala	Glu	Val	Gln	Glu	Glu	Cys
		115					120					125			

Tyr	Ser	Lys	Leu	Asn	Val	Cys	Ser	Ile	Ala	Lys	Arg	Asn	Pro	Glu	Ala
	130					135						140			

Ile Thr Glu Val Val Gln Leu Pro Asn His Phe Ser Asn Arg Tyr Tyr  
 145 150 155 160

Asn Arg Leu Val Arg Ser Leu Leu Glu Cys Asp Glu Asp Thr Val Ser  
 165 170 175

Thr Ile Arg Asp Ser Leu Met Glu Lys Ile Gly Pro Asn Met Ala Ser  
 180 185 190

Leu Phe His Ile Leu Gln Thr Asp His Cys Ala Gln Thr His Pro Arg  
 195 200 205

Ala Asp Phe Asn Arg Arg Arg Thr Asn Glu Pro Gln Lys Leu Lys Val  
 210 215 220

Leu Leu Arg Asn Leu Arg Gly Glu Glu Asp Ser Pro Ser His Ile Lys  
 225 230 235 240

Arg Thr Ser His Glu Ser Ala  
 245

<210> 3  
 <211> 256  
 <212> PRT  
 <213> Oncorhynchus kisutch

<400> 3

Met Leu Ala Lys Phe Gly Leu Cys Ala Val Phe Leu Val Leu Gly Thr  
 1 5 10 15

Ala Ala Thr Phe Asp Thr Asp Pro Glu Glu Ala Ser Pro Arg Arg Ala  
 20 25 30

Arg Phe Ser Ser Asn Ser Pro Ser Asp Val Ala Arg Cys Leu Asn Gly  
 35 40 45

Ala Leu Ala Val Gly Cys Gly Thr Phe Ala Cys Leu Glu Asn Ser Thr  
 50 55 60

Cys Asp Thr Asp Gly Met His Asp Ile Cys Gln Leu Phe Phe His Thr  
 65 70 75 80

Ala Ala Thr Phe Asn Thr Gln Gly Lys Thr Phe Val Lys Glu Ser Leu  
 85 90 95

Arg Cys Ile Ala Asn Gly Val Thr Ser Lys Val Phe Gln Thr Ile Arg  
100 105 110

Arg Cys Gly Val Phe Gln Arg Met Ile Ser Glu Val Gln Glu Glu Cys  
115 120 125

Tyr Ser Arg Leu Asp Ile Cys Gly Val Ala Arg Ser Asn Pro Glu Ala  
130 135 140

Ile Gly Glu Val Val Gln Val Pro Ala His Phe Pro Asn Arg Tyr Tyr  
145 150 155 160

Ser Thr Leu Leu Gln Ser Leu Leu Ala Cys Asp Glu Glu Thr Val Ala  
165 170 175

Val Val Arg Ala Gly Leu Val Ala Arg Leu Gly Pro Asp Met Glu Thr  
180 185 190

Leu Phe Gln Leu Leu Gln Asn Lys His Cys Pro Gln Gly Ser Asn Gln  
195 200 205

Gly Pro Asn Ser Ala Pro Ala Gly Trp Arg Trp Pro Met Gly Ser Pro  
210 215 220

Pro Ser Phe Lys Ile Gln Pro Ser Met Arg Gly Arg Asp Pro Thr His  
225 230 235 240

Leu Phe Ala Arg Lys Arg Ser Val Glu Ala Leu Glu Arg Val Met Glu  
245 250 255

<210> 4  
<211> 733  
<212> DNA  
<213> Homo sapiens

<400> 4  
gggatccgga gcccaaattct tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 60  
aattcgaggg tgcaccgtca gtcttctctt tcccccaaa acccaaggac accctcatga 120  
tctcccgga ccttgaggtc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg 180  
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240  
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300  
ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg 360  
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420

catccccggga' tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct 480  
atccaagcga catcgccgtg gagggggaga gcaatgggca gccggagaac aactacaaga 540  
ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag ctcaccgtgg 600  
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660  
acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720  
gactctagag gat 733

<210> 5  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Contains a SphI restriction enzyme site.

<400> 5  
gactgcatgc tccaaaactc agcagtg 27

<210> 6  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Contains complementary sequences to a BglII restriction site.

<400> 6  
gactagatct tgcactctca tgggatgtgc g 31

<210> 7  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Contains a BamHI restriction enzyme site followed by 6 nucleotide  
s resembling an efficient signal for the initiation of translatio  
n in eukaryotic cells.

<400> 7  
cagtggtatcc gccaccatgc tccaaaactc agcagtg 37

<210> 8  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Contains the cleavage site for the restriction endonuclease Asp71  
8.

<400> 8  
 cagtgggtacc ggttgtgaat aacctctccc 30

<210> 9  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Contains a BamHI restriction enzyme site followed by 6 nucleotide  
 s resembling the efficient signal for translation.

<400> 9  
 cagtggatcc gccaccatgc tccaaaaactc agcagtg 37

<210> 10  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Contains the cleavage site for the restriction endonuclease BamHI

<400> 10  
 cagtggatcc ggttgtgaat aacctctccc 30

<210> 11  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for PCR amplification of the EGR-1 promoter sequence.

<400> 11  
 gcgctcgagg gatgacagcg atagaacccc gg 32

<210> 12  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for PCR amplification of the EGR-1 promoter sequence.

<400> 12  
 gcgaagcttc gcgactcccc ggatccgcct c 31